



**Reply to the Comment on “Quantitative biochronology of the
Permian–Triassic boundary in South China based on conodont unitary
associations”**

Brosse, Morgane ; Bucher, Hugo ; Goudemand, Nicolas

Abstract: 1. Introduction In their Comment, Jiang et al. (2016) claim that the discordance between our zonation (Brosse et al., 2016) and the interval zones does not rest on the use of the Unitary Association method (Guex, 1991 and Guex et al., 2015) per se but on our “failure to use the most recent published conodont ranges from some key Chinese sections”. They add that our analysis is based on “unreliable taxonomic data sets with unjustified taxonomic re-assessments”, and hence, that we did not demonstrate that the Unitary Association method performs better than traditional interval zones. Additionally, the Comment by Jiang et al. (2016) contains misunderstandings pertaining to the method used in our study (Brosse et al., 2016). Our goal was to apply the Unitary Association Method on a dataset of conodont distributions from South China around the Permian–Triassic boundary (PTB) in order to reassess the quality of the corresponding data and to provide a discrete and robust alternative zonation to the continuous, First-Occurrence-based interval zones. Such interval zones are routinely utilized in Permian and Triassic conodont biostratigraphy, regardless of their abundant internal contradictions. Three categories of points of contention can be extracted from the Comment of Jiang et al. (2016): method, selection of data and taxonomy, and illustrations. Each of these is addressed separately below. 2. Method Fig. 1 complies with the recommendation of Jiang et al. (2016) and takes into account all the recent literature, summarizing the most recent published conodont ranges from the relevant sections. The reader will immediately observe that the sequences of First Occurrences (FOs) used in the most recently published interval zones occupy contradictory positions between the different sections. This is precisely the main criticism expressed in our work. This problem cannot be solved by simply standardizing the taxonomy of the considered taxa. Many contradictions do persist after taxonomic homogenization. As conceded by Jiang et al. (2016), FOs are prone to diachronism. But contrary to what Jiang et al. (2016) suggest, sampling effort is not the only nor the main reason for such diachronism and PTB sections from South China are no exceptions in this respect. Fig. 9 of Brosse et al. (2016) demonstrates the contrary. Ironically enough, Jiang et al. (2016) acknowledge that Last Occurrences (LOs) can be diachronous because of local, ecological differences, but they exclude that FOs can be affected. In reality, these authors unduly equate every local FO with an alleged instantaneous spreading of a species across all sections. Incidentally, such an unwarranted assumption also deliberately ignores that speciation is an intrinsically space-restricted evolutionary process.

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Reply to the Comment on “Quantitative biochronology of the Permian–Triassic boundary in South China based on conodont unitary associations”

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Introduction

In their Comment, Jiang et al. (2016) claim that the discordance between our zonation (Brosse et al., 2016) and the interval zones does not rest on the use of the Unitary Association method (Guex 1991, Guex et al. 2015) *per se* but on our “failure to use the most recent published conodont ranges from some key Chinese sections”. They add that our analysis is based on “unreliable taxonomic data sets with unjustified taxonomic re-assessments”, and hence, that we did not demonstrate that the Unitary Association method performs better than traditional interval zones.

Additionally, the comment by Jiang et al. (2016) contains misunderstandings pertaining to the method used in our study (Brosse et al., 2016). Our goal was to apply the Unitary Association Method on a dataset of conodont distributions from South China around the Permian-Triassic boundary (PTB) in order to reassess the quality of the corresponding data and to provide a discrete and robust alternative zonation to the continuous, First-Occurrence-based interval zones. Such interval zones are routinely utilized in Permian and Triassic conodont biostratigraphy, regardless of their abundant internal contradictions.

Three categories of points of contention can be extracted from the comment of Jiang et al. (2016): method, selection of data and taxonomy, and illustrations. Each of these is addressed separately below.

1. Method

Figure 1 complies with the recommendation of Jiang et al. (2016) and takes into account all the recent literature, summarizing the most recent published conodont ranges from the relevant sections. The reader will immediately observe that the sequences of First Occurrences (FOs) used in the most recently published interval zones occupy contradictory positions between the different sections. This is precisely the main criticism expressed in our work. This problem cannot be solved by simply standardizing the taxonomy of the considered taxa. Many contradictions do persist after taxonomic homogenization. As conceded by Jiang et al. (2016), FOs are prone to diachronism. But contrary to what Jiang et al. (2016) suggest, sampling effort is not the only nor the main reason for such diachronism and PTB sections from South China are no exceptions in this respect. Figure 9 of Brosse et al. (2016) demonstrates the contrary. Ironically enough, Jiang et al. (2016) acknowledge that Last Occurrences (LOs) can be diachronous because of local, ecological differences, but they exclude that FOs can be affected. In reality, these authors unduly equate every local FO with an alleged instantaneous spreading of a species across all sections. Incidentally, such an

unwarranted assumption also deliberately ignores that speciation is an intrinsically space-restricted evolutionary process.

Contradictions in the superpositional relationships of FOs prevent *reliable* correlations between sections. The main points in using the Unitary Association method are that (1) one can quantitatively assess the quality of the data, in particular one can detect contradictions, even subtle ones implying three or four taxa in circular or sub-circular relationships; (2) one can iteratively use the information drawn from the detected contradictions to critically reassess the quality of the data, occasionally pointing out previously unseen sampling or taxonomic determination biases; (3) one can drastically reduce the impact of diachronism of single taxa on the resulting zonation by considering only maximal associations of taxa; and (4) all constructed biozones are defined in an exclusive way, i.e. by the occurrence of a characteristic taxon or the co-occurrence of characteristic pairs of taxa. For all these reasons, we consider the Unitary Association method as the single major conceptual and practical advance in the field of biochronology during the last three decades. In particular, we consider that the accuracy (understood as trueness of the results) of the resulting zonation is greatly improved.

The improvement in terms of accuracy and robustness may come with a reduction of the “resolution”, but it must be noted that the “resolution” obtained with interval zones is misleading in that it only represents a very local measure on which no constraint on lateral reproducibility is applied. As opposed to this, poorly laterally reproducible preliminary Unitary Associations can be merged optimally to ensure that the resulting Unitary Association Zones are laterally reproducible, i.e., that the resulting zones can be effectively employed to build robust correlations between sections.

This advance also comes with the recognition that some beds do not contain enough information to be unequivocally dated. Those beds lie within so-called intervals of separation and reflect the amount of undefined and contradictory stratigraphic relations present in each dataset. Contrary to the comment of Jiang et al. (2016), the fact that a boundary such as the PTB lies within an interval of separation does not at all imply that it is not precisely located or defined. Thicknesses of intervals of separation tend to correlate negatively with the density of biostratigraphic relations contained in the data set. Only with Unitary Associations will the biostratigrapher be directly confronted to the quality of the data to be processed and its potential consequences. The user will be forced to acknowledge that some data sets can be partly or completely under-constrained and thus inappropriate for constructing zones having constant superposition order and broad lateral reproducibility. Unitary Associations advance the field of biochronology to an unprecedented point where data can be carefully and quantitatively evaluated, where data sets are amenable to optimization and where a measurable degree of uncertainty can be assigned to a biozonation. In contrast and per definition, interval zones have no uncertainty and form a frozen succession of continuous zones.

2. Selection criteria and taxonomy

Jiang et al. (2016) misunderstood the selection criteria used for the construction of our data set. Only publications with raw range charts and adequate illustrations of documented taxa were taken into account. The “missing” papers mentioned in the comment were not included in our dataset because they did not meet with the above-mentioned criteria. Chen et al. (2015) do not provide any illustrations of conodonts, nor a detailed range chart. The range chart of Zhang et al. (2009) cannot be used because illustrations of taxonomic assignments are lacking: their 16 conodont photographs are in fact copied from Zhang et al. (1995), Yin et al. (2001), and Zhang et al. (2007), and are reproduced without any citation of original sources.

Liu et al. (2007) provide too few illustrations for assessing their taxonomic assignments and the study of Chen et al. (2009) must therefore be preferred for the Dawen section. The range chart of Jiang et al. (2015; see their Fig. 2) is based on that of Yan et al. (2013), which is included in our data set. Contrary to a statement made in the comment, the data of Jiang et al. (2011) were included in our analysis. Contrary to the claim of Jiang et al. (2016), our data also includes the updated stratigraphical ranges of the considered sections. These include the taxonomic adjustment made by Jiang et al. (2011b) who re-assigned *I. staeschei* sensu Jiang et al. (2007) from the bed 27d at Meishan to *I. huckriedei*, and moved up the *I. staeschei* IZ to bed 28 (see our Table 1 and Appendix A; Brosse et al. 2016). The same applies to *H. changxingensis*, which we correctly placed in bed 26 (after Nicoll et al., 2002) in our model, as shown in Appendix A.

3. Illustrations

We thank Jiang et al. (2016) for spotting a typo in the illustration of the holotype of *Isarcicella lobata* in figure 1.10 of Brosse et al. (2016). Our figure 1.10 reproduces the illustration of “*I. lobata* morphotype 1” of Perri and Farabegoli (2003; pl. 3, figs. 27-29). The holotype of *I. lobata* is illustrated by Perri and Farabegoli (2003) in their plate 3, figs. 21-23, to which the reader is now correctly referred.

A graphic typo is also correctly found in figures 9, 10 and 15. In Meishan, the dashed line separating the Changxing and Yinkeng formations is correctly placed between beds 24 and 25. Graphic misplacement of this boundary has absolutely no influence on the validity of our biochronological results.

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Caption

Figure 1: Biostratigraphical correlations of the Wuzhuan, Dajiang, Dawen, Shangsi, Yangou and Meishan sections by means of first occurrences (FOs). The vertical scale (stratigraphical thickness in metres) is the same for the six sections. The 0 on the picture refers to the lithological boundary. *H*: *Hindeodus*, *I*: *Isarcicella*, *N*: *Neogondolella*.

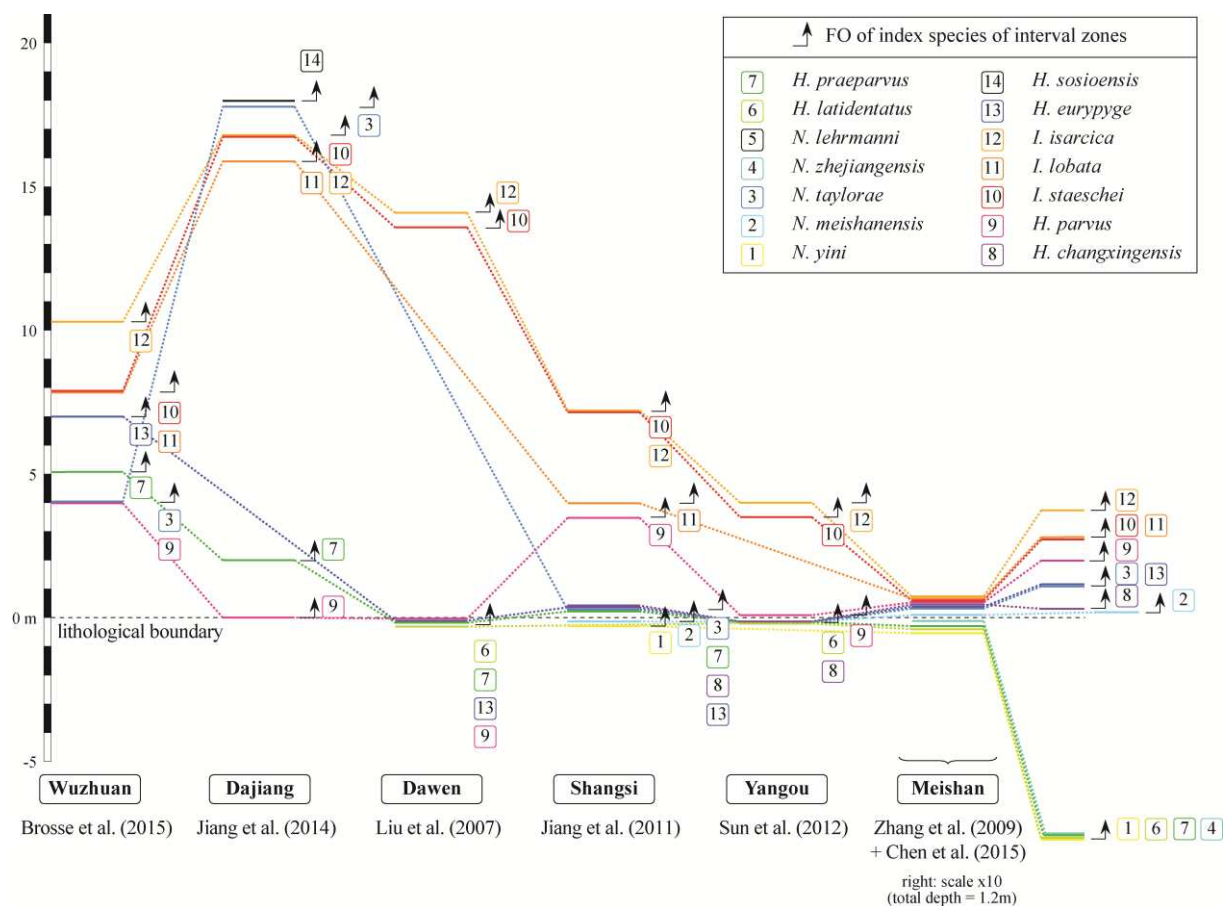


Fig. 1

Appendix A

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

							(3 - 5)
DJG 0.73-0.75	4	1	1	1		1	3
DJG 0.58-0.73		1	1	1		1	3
DJG 0.45-0.5				1		1	2-4 (2 - 3)
DJG 005	3	1		1		1	1-2
DJG 0.15-0.2		1		1		1	1-2
DJG 007		1		1		1	1-2
DJG 008		1		1		1	1-2
DJG 009		1		1		1	1-2
DJG 011		1		1		1	1-2
DJG 012		1		1		1	1-2
DJG 013	2	1		1		1	1-2
DJG 014		1		1		1	2-4 (1 - 2)
DJG - 15.5				1		1	1-4 (1 - 2)

	DJG -19	1	1	1-4 (1-2)
	DJG -21	1	1	1-4 (1-2)
	DJG -32	1	1	1-4 (1-2)
	DJG -35.1	1	1	1-4 (1-2)
	DJG -39.3	1	1	1-4 (1-2)
	DJG -43.8	1	1	1-4 (1-2)
	DJG -49.5	1	1	1-4 (1-2)
	DJG -53.6	1	1	1-4 (1-2)

DJG - 60.9		1	1	1-4 (1-2)
DJG - 66.6		1		1-4 (1-2)
DJG - 70.8	1	1	1	1-2
DJG - 75.8		1	1	1-2
DJG -80		1	1	1-2
DJG -82		1	1	1-2
DJG -85		1	1	1-2
DJG - 88.2		1		1-5 (1-2)
DJG -91		1		1-5 (1-2)
DJG -98		1		1-5 (1-2)
DJG +24.3		1		1-5 (1-2)

[illegible]

[illegible]

	C6-2				1			1	1			1		1-4
	C6-1				1			1	1			1		1-4
	C4-6				1			1	1			1		1-4
	C4-5				1			1	1			1		1-4
	C4-4				1			1	1			1		1-4
	C4-3				1			1	1			1		1-4
	C2-4				1			1	1					1-4
	C1-7				1			1	1					1-4
	C1-3				1			1	1					1-4
	C1-2				1			1	1					1-4
	C1-1				1			1	1					1-4
	C0-2				1			1	1					1-4
Cha otia n	H59	5	1		1	1		1						5
	H55	4			1			1						4-6 (5)
	G9				1									3-6
	F12				1									3-6
	F1				1									3-6
	D24							1	1	1		1	1	2-3
	D22	3						1	1	1		1	1	2-3

C5			1	1	1	1	1	2
C3			1	1	1	1	1	1- 2
C1			1	1	1	1	1	1- 2
B3			1			1		1- 2